REMARKS

Applicant wishes to thank Examiner Lucas for the courtesy extended to Nancy Vensko, attorney of record, on June 22, 2005. The proposed claim language and its application to the cited prior art was discussed. Thus is summarized the discussion held at the telephonic Informal Communication.

A. Disposition of Claims

The invention is related to the complete nucleotide sequence of the core gene of 52 HCV isolates that represent 14 genotypes, the core gene sequences of 9 genotypes having not been previously reported (i.e., genotypes 2c, 4a-f, 5a and 6a). By this amendment, Applicant has amended Claims 4, 5, 11, 15, 16, and 19 to comply with the rules that govern claims formalities and Claims 32 and 38 to make explicit that which was implicit in the claims, and thus all for reasons unrelated to patentability. No claims have been added or deleted. Thus, Claims 4, 5, 11-16, 19, 32-44, and 46 are pending. No new matter has been added. Reexamination and reconsideration of the applications, as amended, are respectfully requested.

B. Compliance with Rules That Govern Claims Formalities

The Patent Office objected to Claims 4 and 5 because these claims encompass "the" full length protein, as opposed to Claims 32 and 38 that refer to any of various different peptides, thus correction in the form of deleting the indefinite article and replacing it with the definite article was required. The claims must comply with the rules that govern claims formalities. Claims 4, 5, 11, 15, 16, and 19 have been amended to delete the indefinite article (or equivalent) and replace it with the definite article. The conclusion is that the claims are in compliance with the rules that govern claims formalities.

C. Compliance with 35 USC § 102

The issue is whether the claims are in compliance with 35 USC § 102. The rule according to MPEP 2131 is that to anticipate a claim, the reference must teach every element of the claim. Here, none of the references teaches every element of any of the claims. The claims were previously amended to define the terms "genotype-specific" as opposed to "universally conserved". Recall that support is found in the Specification at page 15, lines 18-33. Applicant remarked that universally conserved peptides could be deduced by one of ordinary skill in the art at the time of the invention from the amino acids shown in capital letters in the consensus sequence shown in Figure 7J as being conserved among all genotypes. Likewise, Applicant

remarked that genotype-specific peptides could be deduced by one of ordinary skill in the art at the time of the invention from the amino acids shown in lower case in the consensus sequence shown in Figure 7J as being variable within the genotype. Notwithstanding the above, it should be noted that, for a genotype-specific peptide, the peptide must additionally, by definition, be specific to a single genotype, here, the single genotype 6a (type 6) of HCV with reference to Figure 7J, that is, the type having the sequence of SEQ ID NO: 206, because the peptides of the claims were restricted to the elected species of the core protein of SEQ ID NO: 206 and peptides thereof. The grouping of genotype 6a into type 6 of HCV is explained on page 37, lines 8-31, of the Specification, as reproduced below for the convenience of the Examiner:

> The grouping of SEQ ID NOs:103-154 into 14 HCV genotypes is shown below.
>
> | SEQ ID NOs: | Genotypes |
> |---|---|
> | 103-108 | I/1a |
> | 109-124 | II/1b |
> | 125-128 | III/2a |
> | 129-133 | IV/2b |
> | 134 | 2c |
> | 135-138 | V/3a |
> | 139 | 4a |
> | 141 | 4b |
> | 143 | 4c |
> | 144 | 4c |
> | 145 | 4d |
> | 142 | 4e |
> | 140 | 4f |
> | 146-153 | 5a |
> | 154 | 6a |
>
> These 14 genotypes can be further grouped into 6 major genotypes designated genotypes 1-6 where genotype 1 comprises the sequences contained in minor genotypes I/1a and II/1b; genotype 2 comprises the sequences contained in minor genotypes III/2a, IV/2b and 2c; genotype 3 comprises sequences contained in genotype V/3a; genotype 4 comprises sequences contained in minor genotypes 4a-4f; genotype 5 comprises the sequences contained in genotype 5a and genotype 6 comprises the sequence contained in genotype 6a.

Additionally, the term "having" in Claims 32 and 38 has been amended to conform to the definitions. On the one hand, the genotype-specific peptide comprises (open language) an amino acid sequence of at least 8 amino acids deduced from genotype-specific amino acid domains located in SEQ ID NO: 206, because, by definition, the peptide is specific to genotype 6a and the sequence of this genotype had not previously been reported. On the other hand, the universally conserved peptide consists of (closed language) an amino acid sequence of at least 8 amino acids deduced from universally conserved amino acid domains found in SEQ ID NO: 206, because, by definition, the peptide is conserved and the sequences of several of the other genotypes had previously been reported.

Let us now turn to the references themselves, where it will be seen that the claims, no matter whether drawn to "genotype-specific" or "universally conserved" peptides, do not encompass a single prior art peptide. Beginning with DeLeyes et al. (see EXHIBIT 1), the claims drawn to "universally conserved" peptides do not read on either DeLeyes Peptide IIa (aa 8 to 18 of SEQ ID NO: 206) or DeLeyes Peptide IV (aa 37 to 56 of SEQ ID NO: 206) because the reference peptide does not consist of an amino acid sequence of at least 8 amino acids deduced from universally conserved amino acid domains found in SEQ ID NO: 206. The amino acids are not all universally conserved. This is because the amino acids are not shown in all capital letters in the consensus sequence shown in Figure 7J as being conserved among all genotypes. Moreover, the claims drawn to "genotype-specific" peptides do not read on either DeLeyes Peptide IIa (aa 8 to 18 of SEQ ID NO: 206) or DeLeyes Peptide IV (aa 37 to 56 of SEQ ID NO: 206) because the reference peptide does not comprise an amino acid sequence of at least 8 amino acids deduced from genotype-specific amino acid domains located in SEQ ID NO: 206. The amino acids are not specific to genotype 6a. This is because any amino acid sequence of at least 8 amino acids located in the reference peptide is also located in at least one of the other genotypes.

Referring to Ferroni et al. (see EXHIBIT 2), the claims drawn to "universally conserved" peptides do not read on either Ferroni Peptide G15V (aa 32 to 46 of SEQ ID NO: 206) or Ferroni Peptide R15P (aa 50 to 64 of SEQ ID NO: 206) because the reference peptide does not consist of an amino acid sequence of at least 8 amino acids deduced from universally conserved amino acid domains found in SEQ ID NO: 206. The amino acids are not all universally conserved. This is because the amino acids are not shown in all capital letters in the consensus sequence shown in

Figure 7J as being conserved among all genotypes. Moreover, the claims drawn to "genotype-specific" peptides do not read on either Ferroni Peptide G15V (aa 32 to 46 of SEQ ID NO: 206) or Ferroni Peptide R15P (aa 50 to 64 of SEQ ID NO: 206) because the reference peptide does not comprise an amino acid sequence of at least 8 amino acids deduced from genotype-specific amino acid domains located in SEQ ID NO: 206. The amino acids are not specific to genotype 6a. This is because any amino acid sequence of at least 8 amino acids located in the reference peptide is also located in at least one of the other genotypes.

Referring to Chien et al. (see EXHIBIT 3), the claims drawn to "universally conserved" peptides do not read on Chien Peptide of SEQ ID NO: 30 (extending from aa 15 to 45 of SEQ ID NO: 206 but differing at aa position 20) because the reference peptide does not consist of an amino acid sequence of at least 8 amino acids deduced from universally conserved amino acid domains found in SEQ ID NO: 206. The amino acids are not all universally conserved. This is because the amino acids are not shown in all capital letters in the consensus sequence shown in Figure 7J as being conserved among all genotypes. Moreover, the claims drawn to "genotype-specific" peptides do not read on Chien Peptide of SEQ ID NO: 30 because the reference peptide does not comprise an amino acid sequence of at least 8 amino acids deduced from genotype-specific amino acid domains located in SEQ ID NO: 206. The amino acids are not specific to genotype 6a. This is because any amino acid sequence of at least 8 amino acids located in the reference peptide is also located in at least one of the other genotypes.

Referring to Miyamura et al. (see EXHIBIT 4), the claims drawn to "universally conserved" peptides do not read on Miyamura Peptide of FIG. 1 (extending from aa 1 to 154 of SEQ ID NO: 206 but differing at aa position 4, 20, 70, 72, 75, 89, 91, 106, 139, 146, 147, and 149) because the reference peptide does not consist of an amino acid sequence of at least 8 amino acids deduced from universally conserved amino acid domains found in SEQ ID NO: 206. The amino acids are not all universally conserved. This is because the amino acids are not shown in all capital letters in the consensus sequence shown in Figure 7J as being conserved among all genotypes. Moreover, the claims drawn to "genotype-specific" peptides do not read on Miyamura Peptide of FIG. 1 because the reference peptide does not comprise an amino acid sequence of at least 8 amino acids deduced from genotype-specific amino acid domains located in SEQ ID NO: 206. The amino acids are not specific to genotype 6a. This is because any amino

acid sequence of at least 8 amino acids located in the reference peptide is also located in at least one of the other genotypes.

In view of the foregoing, the conclusion is that the references fail to anticipate the claims, thus the claims are in compliance with 35 USC § 102.

D. Compliance with 35 USC § 103

The issue is whether the claims are in compliance with 35 USC § 103. The rule according to MPEP 2143 is that the prior art references must teach or suggest all the claim limitations and there must be some suggestion or motivation in the prior art to combine the references. Here, neither primary reference Chien (as described above) nor Miyamura (as described above) describe or suggest "genotype-specific" or "universally conserved" peptides as defined in the claims. Moreover, the secondary reference of Li et al. (of the previous office action) cannot fill in the gaps, because the invention is related to the complete nucleotide sequence of the core gene of 52 HCV isolates that represent 14 genotypes, the core gene sequences of 9 genotypes having not been previously reported (i.e., genotypes 2c, 4a-f, 5a and 6a). The missing sequences are empirical and thus nonobvious. The conclusion is that the claims are in compliance with 35 USC § 103.

CONCLUSION

In view of the above, it is submitted that the claims are in condition for allowance. Reconsideration and withdrawal of all outstanding rejections are respectfully requested. Allowance of the claims at an early date is solicited. If any points remain that can be resolved by telephone, the Examiner is invited to contact the undersigned at the below-given telephone number.

Respectfully submitted,

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